Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:15 AM GMT

PDB ID	:	2Q1T
Title	:	Crystal structure of the Bordetella bronchiseptica enzyme WbmF in complex with NAD+ and UDP
Authors	:	Harmer, N.J.; King, J.D.; Palmer, C.M.; Maskell, D.; Blundell, T.L.
Deposited on	:	2007-05-25
Resolution	:	1.75 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see references ⓘ) were used in the production of this report:

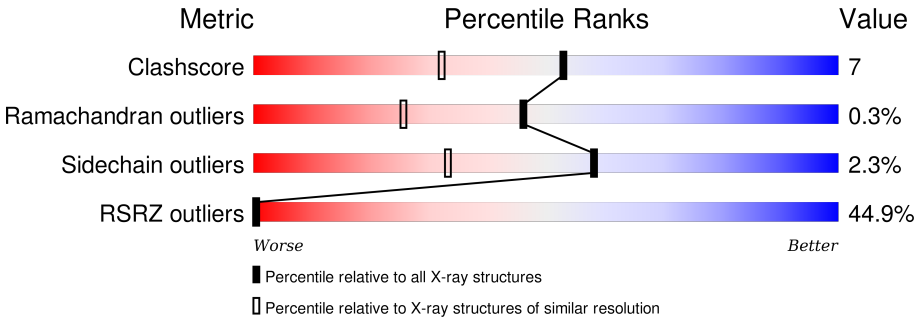
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	1730 (1.76-1.76)
Ramachandran outliers	100387	1711 (1.76-1.76)
Sidechain outliers	100360	1711 (1.76-1.76)
RSRZ outliers	91569	1610 (1.76-1.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	377	40% 79% 8% • 12%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2834 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

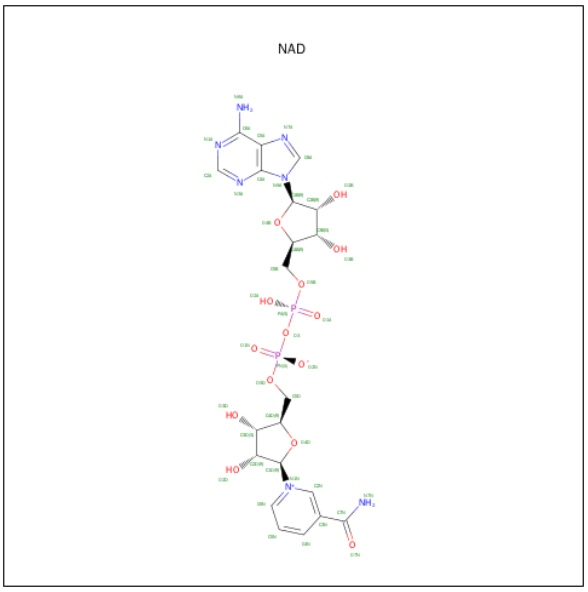
- Molecule 1 is a protein called Putative nucleotide sugar epimerase/ dehydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	332	Total	C	N	O	S	0	3	0
			2556	1622	442	487	5			

There are 20 discrepancies between the modelled and reference sequences:

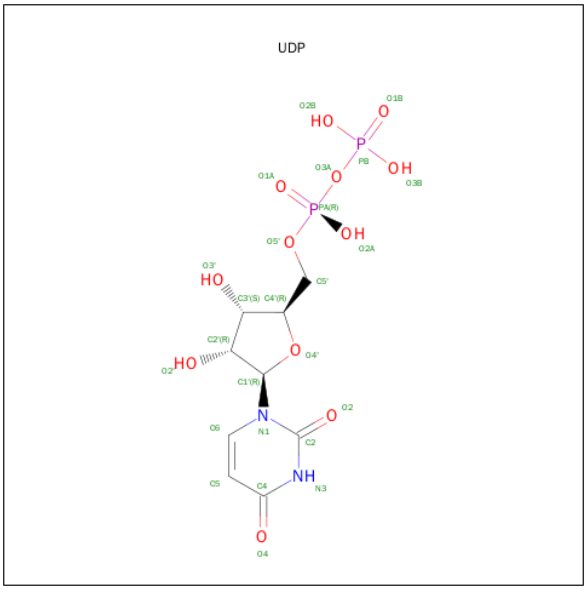
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP O87989
A	-18	GLY	-	EXPRESSION TAG	UNP O87989
A	-17	SER	-	EXPRESSION TAG	UNP O87989
A	-16	SER	-	EXPRESSION TAG	UNP O87989
A	-15	HIS	-	EXPRESSION TAG	UNP O87989
A	-14	HIS	-	EXPRESSION TAG	UNP O87989
A	-13	HIS	-	EXPRESSION TAG	UNP O87989
A	-12	HIS	-	EXPRESSION TAG	UNP O87989
A	-11	HIS	-	EXPRESSION TAG	UNP O87989
A	-10	HIS	-	EXPRESSION TAG	UNP O87989
A	-9	SER	-	EXPRESSION TAG	UNP O87989
A	-8	SER	-	EXPRESSION TAG	UNP O87989
A	-7	GLY	-	EXPRESSION TAG	UNP O87989
A	-6	LEU	-	EXPRESSION TAG	UNP O87989
A	-5	VAL	-	EXPRESSION TAG	UNP O87989
A	-4	PRO	-	EXPRESSION TAG	UNP O87989
A	-3	ARG	-	EXPRESSION TAG	UNP O87989
A	-2	GLY	-	EXPRESSION TAG	UNP O87989
A	-1	SER	-	EXPRESSION TAG	UNP O87989
A	0	HIS	-	EXPRESSION TAG	UNP O87989

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula: $C_9H_{14}N_2O_{12}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			25	9	2	12	2		

- Molecule 4 is water.

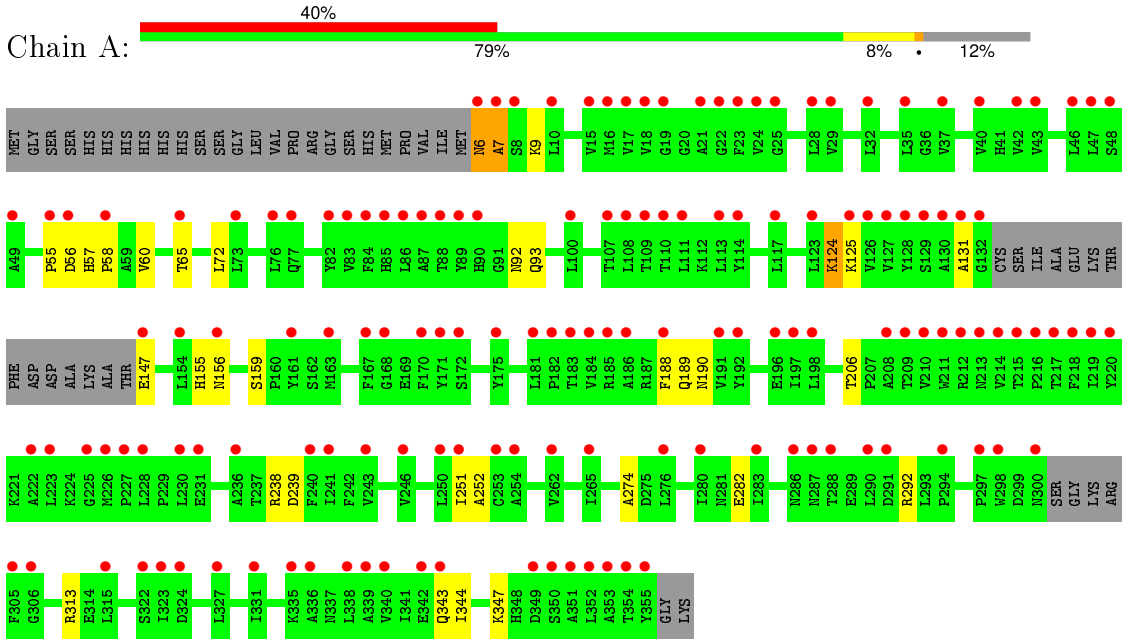
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	209	Total	O	0	0
			209	209		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Putative nucleotide sugar epimerase/ dehydratase

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	83.44Å 78.12Å 59.26Å 90.00° 108.08° 90.00°	Depositor
Resolution (Å)	28.52 – 1.75 23.51 – 1.75	Depositor EDS
% Data completeness (in resolution range)	93.2 (28.52-1.75) 93.2 (23.51-1.75)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.85 (at 1.76Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.183 , 0.219 0.181 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å^2)	26.7	Xtriage
Anisotropy	0.135	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 33.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 33887 reflections	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	2834	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.64% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UDP, NAD

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.74	0/2619	0.73	1/3562 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	56	ASP	CB-CG-OD2	5.38	123.15	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2556	0	2488	34	0
2	A	44	0	26	5	0
3	A	25	0	11	2	0
4	A	209	0	0	5	0
All	All	2834	0	2525	34	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (34) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6:ASN:HB3	1:A:251:ILE:HG22	1.34	1.03
1:A:190:ASN:OD1	4:A:498:HOH:O	1.98	0.81
1:A:6:ASN:HA	1:A:252:ALA:HA	1.62	0.80
1:A:239:ASP:OD1	4:A:498:HOH:O	2.00	0.80
1:A:65[B]:THR:OG1	1:A:72:LEU:HD12	1.82	0.80
1:A:57:HIS:ND1	1:A:58:PRO:HD2	2.00	0.76
1:A:7:ALA:HB2	4:A:474:HOH:O	1.86	0.76
1:A:6:ASN:HB3	1:A:251:ILE:CG2	2.17	0.73
1:A:344:ILE:O	1:A:347:LYS:HG2	1.98	0.63
1:A:72:LEU:C	1:A:72:LEU:HD23	2.28	0.54
1:A:188:PHE:O	2:A:358:NAD:H5N	2.09	0.53
1:A:189:GLN:HA	2:A:358:NAD:H4N	1.93	0.51
1:A:188:PHE:O	2:A:358:NAD:C5N	2.59	0.51
1:A:55:PRO:HG2	1:A:60:VAL:HG21	1.93	0.50
1:A:6:ASN:HA	1:A:252:ALA:CA	2.39	0.49
1:A:238:ARG:NH2	3:A:400:UDP:O1B	2.40	0.49
1:A:65[B]:THR:OG1	1:A:72:LEU:CD1	2.58	0.47
1:A:131:ALA:HA	2:A:358:NAD:H6N	1.99	0.45
1:A:238:ARG:HE	3:A:400:UDP:PA	2.40	0.45
1:A:147:GLU:HG2	4:A:508:HOH:O	2.17	0.44
1:A:6:ASN:CB	1:A:251:ILE:HG22	2.25	0.44
1:A:124:LYS:HD3	1:A:124:LYS:N	2.32	0.44
1:A:6:ASN:HB2	1:A:7:ALA:H	1.26	0.44
1:A:57:HIS:CG	1:A:58:PRO:HD2	2.52	0.43
1:A:189:GLN:HA	2:A:358:NAD:C4N	2.48	0.43
1:A:155:HIS:O	1:A:156:ASN:HB2	2.18	0.43
1:A:6:ASN:O	1:A:7:ALA:HB2	2.19	0.42
1:A:274:ALA:HB1	1:A:292:ARG:HG2	2.02	0.42
1:A:7:ALA:HB1	1:A:9:LYS:H	1.85	0.41
1:A:93:GLN:HE21	1:A:206:THR:CB	2.33	0.41
1:A:7:ALA:CB	1:A:9:LYS:H	2.34	0.40
1:A:57:HIS:HB3	1:A:60:VAL:HB	2.03	0.40
1:A:156:ASN:HB2	4:A:572:HOH:O	2.20	0.40
1:A:92:ASN:ND2	1:A:159:SER:OG	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	329/377 (87%)	322 (98%)	6 (2%)	1 (0%)	46 25

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	7	ALA

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	267/315 (85%)	261 (98%)	6 (2%)	60 35

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ASN
1	A	124	LYS
1	A	125	LYS
1	A	282	GLU
1	A	313	ARG
1	A	343	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	92	ASN
1	A	93	GLN
1	A	103	HIS
1	A	156	ASN
1	A	178	GLN
1	A	189	GLN
1	A	343	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAD	A	358	-	38,48,48	1.66	3 (7%)	47,73,73	1.95	9 (19%)
3	UDP	A	400	-	18,26,26	1.26	1 (5%)	26,40,40	1.59	3 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	A	358	-	-	0/22/62/62	0/5/5/5
3	UDP	A	400	-	-	0/12/32/32	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	358	NAD	PN-O1N	-2.26	1.42	1.51
2	A	358	NAD	C2A-N3A	3.07	1.37	1.32
3	A	400	UDP	C4-N3	3.25	1.39	1.33
2	A	358	NAD	O7N-C7N	7.88	1.41	1.24

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	358	NAD	N3A-C2A-N1A	-9.13	121.91	128.89
2	A	358	NAD	O7N-C7N-C3N	-3.91	115.32	119.59
3	A	400	UDP	PA-O3A-PB	-3.33	121.49	132.67
2	A	358	NAD	C4A-C5A-N7A	-3.16	106.57	109.48
2	A	358	NAD	C1B-N9A-C4A	-2.42	123.29	126.94
2	A	358	NAD	C4B-O4B-C1B	-2.38	107.11	109.72
2	A	358	NAD	PN-O3-PA	-2.14	126.72	132.73
2	A	358	NAD	O2B-C2B-C3B	2.14	118.80	111.83
2	A	358	NAD	C3N-C7N-N7N	2.26	120.29	117.82
3	A	400	UDP	O3A-PA-O5'	2.32	109.09	102.94
2	A	358	NAD	O3-PA-O5B	2.99	110.86	102.94
3	A	400	UDP	C4-N3-C2	5.92	120.00	114.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	358	NAD	5	0
3	A	400	UDP	2	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	332/377 (88%)	2.15	149 (44%)	0	0	23, 41, 54, 62	0

All (149) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	354	THR	8.2
1	A	287	ASN	8.1
1	A	6	ASN	7.7
1	A	127	VAL	7.5
1	A	84	PHE	7.3
1	A	126	VAL	7.3
1	A	219	ILE	6.8
1	A	198	LEU	6.7
1	A	83	VAL	6.5
1	A	355	TYR	6.5
1	A	353	ALA	6.5
1	A	280	ILE	6.4
1	A	86	LEU	6.2
1	A	128	TYR	5.8
1	A	8	SER	5.8
1	A	339	ALA	5.7
1	A	216	PRO	5.5
1	A	113	LEU	5.4
1	A	351	ALA	5.3
1	A	18	VAL	5.3
1	A	23	PHE	5.2
1	A	7	ALA	5.1
1	A	214	VAL	5.0
1	A	181	LEU	5.0
1	A	227	PRO	4.8
1	A	114	TYR	4.8
1	A	24	VAL	4.8

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Mol	Chain	Res	Type	RSRZ
1	A	156	ASN	4.7
1	A	167	PHE	4.7
1	A	352	LEU	4.7
1	A	288	THR	4.5
1	A	218	PHE	4.5
1	A	32	LEU	4.4
1	A	17	VAL	4.3
1	A	184	VAL	4.3
1	A	65[A]	THR	4.3
1	A	28	LEU	4.2
1	A	250	LEU	4.2
1	A	197	ILE	4.2
1	A	215	THR	4.1
1	A	305	PHE	4.1
1	A	82	TYR	4.0
1	A	210	VAL	3.9
1	A	327	LEU	3.9
1	A	343	GLN	3.9
1	A	87	ALA	3.9
1	A	111	LEU	3.8
1	A	56	ASP	3.8
1	A	265	ILE	3.8
1	A	171	TYR	3.8
1	A	132	GLY	3.7
1	A	217	THR	3.7
1	A	228	LEU	3.6
1	A	331	ILE	3.6
1	A	107	THR	3.6
1	A	186	ALA	3.5
1	A	85	HIS	3.5
1	A	40	VAL	3.5
1	A	276	LEU	3.5
1	A	131	ALA	3.5
1	A	48	SER	3.4
1	A	226	MET	3.4
1	A	10	LEU	3.4
1	A	47	LEU	3.4
1	A	306	GLY	3.4
1	A	110	THR	3.4
1	A	16	MET	3.4
1	A	286	ASN	3.4
1	A	298	TRP	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	130	ALA	3.4
1	A	129[A]	SER	3.4
1	A	251	ILE	3.3
1	A	43	VAL	3.2
1	A	290	LEU	3.2
1	A	15	VAL	3.2
1	A	262	VAL	3.2
1	A	291	ASP	3.1
1	A	29	VAL	3.1
1	A	188	PHE	3.1
1	A	212	ARG	3.1
1	A	58	PRO	3.1
1	A	191	VAL	3.1
1	A	88	THR	3.0
1	A	55	PRO	3.0
1	A	246	VAL	3.0
1	A	254	ALA	3.0
1	A	37	VAL	3.0
1	A	154	LEU	3.0
1	A	117	LEU	2.9
1	A	315	LEU	2.9
1	A	324	ASP	2.9
1	A	42	VAL	2.9
1	A	338	LEU	2.9
1	A	89	TYR	2.8
1	A	297	PRO	2.8
1	A	109	THR	2.8
1	A	350	SER	2.7
1	A	175	TYR	2.7
1	A	241	ILE	2.7
1	A	230	LEU	2.7
1	A	77	GLN	2.7
1	A	225	GLY	2.7
1	A	25	GLY	2.6
1	A	183	THR	2.6
1	A	172	SER	2.6
1	A	125	LYS	2.6
1	A	253	CYS	2.6
1	A	73	LEU	2.6
1	A	322	SER	2.6
1	A	123	LEU	2.6
1	A	161	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	220	TYR	2.6
1	A	108	LEU	2.5
1	A	49	ALA	2.5
1	A	21	ALA	2.5
1	A	163	MET	2.5
1	A	211	TRP	2.5
1	A	240	PHE	2.5
1	A	340	VAL	2.4
1	A	208	ALA	2.4
1	A	213	ASN	2.4
1	A	192	TYR	2.4
1	A	300	ASN	2.4
1	A	185	ARG	2.3
1	A	76	LEU	2.3
1	A	196	GLU	2.3
1	A	100	LEU	2.3
1	A	222	ALA	2.3
1	A	336	ALA	2.3
1	A	147	GLU	2.3
1	A	19	GLY	2.3
1	A	170	PHE	2.3
1	A	342	GLU	2.2
1	A	243	VAL	2.2
1	A	209	THR	2.2
1	A	35	LEU	2.2
1	A	231	GLU	2.2
1	A	46	LEU	2.2
1	A	90	HIS	2.2
1	A	283	ILE	2.2
1	A	323	ILE	2.2
1	A	294	PRO	2.2
1	A	349	ASP	2.1
1	A	223	LEU	2.1
1	A	335	LYS	2.1
1	A	168	GLY	2.1
1	A	236	ALA	2.1
1	A	182	PRO	2.0
1	A	22	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
3	UDP	A	400	25/25	0.76	0.31	1.73	44,46,49,51	8
2	NAD	A	358	44/44	0.96	0.17	-1.22	19,25,41,43	0

6.5 Other polymers (i)

There are no such residues in this entry.